

### **Descriptions of additional supplementary data files**

Supplementary Data 1 Supplementary Data 1 is related to Figure 1. The data include TPP genes identified in MED26 ChIP-seq analysis. Peak calling of MED26 ChIPseq was performed using MACS with the default settings. The MED26 ChIPseq data are deposited in GEO under accession number GSE121024.

Supplementary Data 2 Supplementary Data 2 is related to Figure 4. RNA-seq of ribo-depleted libraries from HEK293T cells and EAF1-mutant cell lines. The data include transcripts exhibiting decreased abundance ( $\log_2 \leq 1$ , adjusted P-value  $\leq 0.01$ ) in ribodepleted libraries. The P values were determined by two-sided Wilcoxon's signed-rank test.